



**FIG. 1 Continued**

[illegible]

**FIG. 1 Continued**

TGCCCCGGGGCTGCGAGCTCCTGTCCAGGAACCGGACACATGTCCGCTGCCAGTGCAGCCACACAGCCAGCTTTGCGGTGC  
TCATGGATATCTCCAGGCGTGAGAACGGGAGGTCTGCCCTCTGAAGATTGTACCTATGCCGCTGTCTCCTTGTCACTG  
GCAGCCCTGCTGCTGGCCTTCCTCTCCTGAGCCTGCTCCGCTGCTGCGCTCCAACCTGCACAGCATTCACAAGCACCT  
CGCCGTGCGCTCTTCTCTCTCAGCTGGTGTTCGTGATTGGGATCAACCAGACGGAAACCCGTTTCTGTGCACAGTGG  
TTGCCATCCTCCTCCACTACATCTACATGAGCACCTTTGCCCTGGACCTCCTGGAGACCTGTCATGTCTACCGCATGCTG  
ACCGAGGTGCCAACATCGACACGGGGCCCATGCGGTCTACTACGTCGTGGGCTGGCGCATCCCGGCCATTGTACAGG  
ACTGGCGGTGCGCCTGGACCCCCAAGGCTACGGGAACCCGACTTCTGCTGGCTGTGCTTCAAGACACCTGATTTGGA  
GCTTTGCGGGGCCCATCGGAGCTGTTATAATCATCAACACAGTCACCTTCTGTCTATCTGCAAAGGTTTCTGCCAAAGA  
AAGCACCATTAATTATGGGAAAAAAGGGATCGTCTCCCTGCTGAGGACCOCATTCTCTGCTGCTGCTCATCAGCGCCAC  
CTGGCTGCTGGGCTGCTGGCTGTGAACCGCGATGCACTGAGCTTTCCTACTACCTCTTCGCCATCTTCAGCGCTTACAGG  
GCCCCCTCGTCTCTCTTTTCCACTGCGTGCTCAACCAGGAGGTCCGGAAACACCTGAAGGGCGTGCTCGGCGGGAGGAAG  
CTGCACCTGGAGGACTCCGCCACACAGGGCCACCCTGCTGACGCGCTCCCTCAACTGCAACACCACCTTCGGTGACGG  
GCTTGACATGCTGCGACAGACTTGGGCGAGTCCACCGCTCCTGAGACAGCATCTGTCAGGGATGAAGGGATCCAGAAGC  
TCGGCGTGTCTCTGGGCTGGTGAGGGGACGCCACGGAGAGCCAGACGCGTCCCTCATGCCCAGGAGCTGCAAGGATCCC  
CCTGGCCACGATTCGCACTCAGATAGCGAGCTGTCCCTGATGAGCAGAGCAGCTCTTACGCTCTCTCACACTCGTCAGA  
CAGCGAGGACGATGGGGTGGGAGCTGAGGAAAAATGGGACCCGGCCAGGGGCGCCGTCCACAGCACCCCAAAGGGGACG  
CTGTGGCCAAACACGTTCCGGCCGGCTGGCCCGACAGAGCTGGCTGAGAGTGACAGTGAGGACCCACAGGGCAAGCCC  
CGCTGAAGGTGGAGACCAAGGTACGCTGGAGCTGCCCGCGAGGAGCAGGGCAGTCACCGTGAGAGTACCCCCCGGA  
CCAGGAGAGCGGGGCGCAGCCAGGCTTGCTAGCAGCCAGCCCCAGAGCAGAGGAAAGGCATCTTGAAAAATAAAGTCA  
CCTACCCGCGCGCTGACGCTGACGGAGCAGAGCTGAAGGGCCGGCTCCGGGAGAAGCTGGCCGACTGTGAGCAGAGC  
CCCACATCCTCGCGACGCTTTCCTGGGCTCTGGCGGGCCCCGACTGCGCCATCACAGTCAAGAGCCCTGGGAGGGAGCC  
GGGCGTGACCACTCAACGGGTGGCCATGAATGTGCGCACTGGGAGCCCCAGGCCGATGGCTCCGACTCTGAGAAAC  
CGTGA

FIG. 2

MAPPPPVFLVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPGCTYAVGAACTPRAPRELLDVGDRGLAGRRRV8  
 CACRPLPLQVRLVARSAPTALSRRRLRARTHLPGCGARARLCGTGARLCGALCFVPGGCAAAQHSALAAPITLPAACRCPP  
 RPRPRCPGRPICLPPGGSVRLRLCALRAAGAVRVGLALEAATAGTPSASPSPPPLPPNLPEARAGPARRARRGTSGR  
 GSLKPPMPNYQVALPENEPAGTLILQLHAYTIEGESEERVSYMEGLFDERBRGYFRIDSATQAVSTDSVLDRETKETHV  
 LRVKAVDYSTPPRSATTYITVLVKDTNDHSVVFQSEYRERVRENLEVGVEVLTIRASDRDSPINANLRYRVLGGAWDV  
 QLNESGCVVSTRAVLDRERAAEYQLLVEANDQGRNPGPLSATATVYIEVEDENDNYPQFSEQNYVVQVPEVDGLNTAVLR  
 VQATDRDQGGONAAIHYSILSGNVAGQFYLHSLSGILDVINPLDFEDVQKYSLSIKAQDGRPPPLINSSGVVSVQVLDVND  
 NEPIFVSSPPQATVLENVPLGYFVVHIQAVDADSGENARLHYRLVDTASTFLGGGSAGPKNPAPTDFPFQIHNSGWT  
 VCAELDREEVEHYSPFGEAVDHGSPPMSSSTSVSITVLVDNDNDFVFTQPTYELRLNEDAAVQSSVLTQLQARDRANSVI  
 TYQLTGGNTRNRFALSSQRGGGLITLALPLDYKQEQYVLAHTASDGTSHHTAHVLINVTANTHRFPVQSSHYTVSVSE  
 DRPVGTSIATLSANDEDTGENARITYVIQDFVPQFRIDPDSGTMYTMMELDYENQVATILTMAQDNGIPKSDTTLLEI  
 LILDANDNAPQFLWDFYQGSIPEDAPPETSILOVSATDRDSCPNORLLYTFQGGDGDGDFYIEPTSGVIRTQRRLDREN  
 VAVYNLWALAVDRGSPTPLSASVEIQVTILDINDNAPHEKDELELFVEENNPFVGSVVAKIRANDPDEGPNAQIMYQIVE  
 GDMRHFPQLDLLNGDLRAMVELDFEVRREYVLVVQATSAPLVSRATVHILLVDQNDNPFVLPDFQILFNMYVTNKSNSFP  
 TQVIGCIPAHDPDVSDSLNYTFVQGNELRLLLLDPATGELQLSRDLDMNRPLEALMEVSVSDGIHSVTAPCTLRVTIITD  
 DMLTNSITVRLNMSQEKFLSPLALFVEGVAAVLSTTKDDVVFVNVQNDTIVSSNINLVTF SALLPGGVGRQGFPSSEDL  
 QEIQIYLNRLTTLTISTQRVLEFFDDNICLREPCENYMKCVSVLRFDSAPFLSSTTVLFRPIHPIINGLRCRCPPGFTGDYC  
 ETEIDLCYSDPCGANGRCRREGGYTCECFEDFTGEHCEVDARSGRGANGVCKNGGTCVNLLIGGFHCVCPPGEYERFPC  
 EVTTRSPFPQSFVTFRGLRQRPHFTISLTFATQERNGLLYNGRFRNEKHDFIALEIVDEQVQLTFSAGETTTTVAPKVP  
 GVSDCRWHSVQVQYNYKPNIGHLGLPHGPGSGEKMAVTVDDCDTMAVRFKDIGNYSCAAQGTQTGSKSLDLTGPLLL  
 GGVNPLPEDFPVHNRQFVGCMRNLSDVGKQVDMAGFIANNQTRREGCAARRNFCGRRRCQNGGTCVNRWNMYLCECPLRF  
 GKNCEQAMPHPQLFSGESVVSWSDLNIIISVFWYLGMLFRTKEDSVLMEATSGGPTSPRLQILNNYLOFEVSHGPSDB  
 SVMLSGLRVTDGEWHLLIELKNVKEDSEMCHLVMTLDYCMDQNKADIGGMPLGLTVRSVVVGGASEDKVSVRRGRFC  
 MQGVRCCTPTNVATLNMNNAKVRVKDGCDDVDPCTSSPCPPNSRCHDAWEDYSCVCDKGYLGINCVDAHLNPCENMO  
 ACVRSPGSPQGYVCECGPSHYGPHYCENKLDLPFCPRGWGNEVFCGPCHCAVSKGFPDPCNKTNQGCQCKENYKLLAQDTC  
 LPCDCFPHGSHSRCTDMATGQCACKPGVIGRQCNRCDNPPAEVTTLGCEVIYNGCPKAFEGAGIWWPQTKFCQPAAVPCPK  
 GSVGNVAVRHCSEKGNLPPPELFNCTTISFVDLRAMNEKLSRNETQVDCARALQVRLARSATQHTGTLPNDVVRTAYQLL  
 GHVLQHSWQGGFDLAATQDADFHEVDVHSCSALLAPATRAAWEQIQRSEGGTAQLLRLECYFSNVARNVARTYLRPFV  
 IVTANMILAVDIFDKFNFTGARVPRFDTIHREFFPRELESSVSFPADFFRPPEEKEGFLLRPAGRRTTPQTRPGPGERE  
 APISRRRRHPDDAGQFAVALVITYRTLQQLLPERYDPDRSLRLPHRPIINTPMVSTLVYSEGAPLPRPLERFVLVEFAL  
 LEVEERTKPVCFVWNHSLAVGGTGGWSARGCELLSRNRTHVACQCSTASPAVLMDISRRENGEVLPLKIVTYAAVSLSL  
 AALLVAPVLLSLVRMLRSNLHSIHKHLAVALFLSQLVVFVIGINQNTENPFCTVVAILLHYIYNSTFAWTLVESLHVYRL

TEVRNIDTQPMRFYYVVGWGIPIAVTGLAVGLDPQGYGNPDCFWSLSQDTLIWSFAGPIGAVIIINTVTSVLSAKVSCQR  
 KHHYYGKKGIVSLLRTAFLLLLISATWLLQLLAVNRDALSFHYLFAIFSGLQGPVLLFHCVLNQEVKHLKGVLGGRK  
 LHLSDSATTRATLLTRSLNCTTTFGDGPDMLRTDLGESTASLDSIVRDEGIQKLGVSGLVRGSHGEPDASLMPSCKDP  
 PCHSDSDSELSLDEQSSSYASSHSSDSEDGVAEEKWDPARGAHVSTPKGDVAVNHVPAGWPDQSLAESDSEDPGKFP  
 RLKVVETKVSVELHREBQSGHREYPPDQESGGARLASSQPPBQRKGILKNKVITYPPFLTLTEQTLKGRLEKLADCEQS  
 PTSSRTSSLSGGGPDCAITVKEPGREFGRDHLANGVAMNVRTGSAQADGSDSEK

**FIG. 3**

Score = 939 (140.9 bits), Expect = 4.0e-81, Sum P(3) = 4.0e-81  
Identities = 203/218 (93%), Positives = 203/218 (93%), Strand = Plus / Plus

Query: 230 CTGTAATAAGACCAACGCCAGTGCCAAT-GCAAGGAGAATTACTACAAGCTCCTAGCCC 288  
CTG A T A A C GCC TG C T GCA GGAGAATTACTACAAGCTCCTAGCCC  
Sbjct: 38281 CTGAAGTCACAGGCCCTGCCCTCTGGCTTTTGCA-GGAGAATTACTACAAGCTCCTAGCCC 38339

Query: 289 AGGACACCTGTCTGCCCTGCCGACTGCTTCCCCCATGGCTCCACAGCCGCACTTGCGACA 348  
AGGACACCTGTCTGCCCTGCCGACTGCTTCCCCCATGGCTCCACAGCCGCACTTGCGACA  
Sbjct: 38340 AGGACACCTGTCTGCCCTGCCGACTGCTTCCCCCATGGCTCCACAGCCGCACTTGCGACA 38399

Query: 349 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGGCGTCATCGGCCGCCAGTGCAACCGCTGCG 408  
TGGCCACCGGGCAGTGTGCCTGCAAGCCCGGCGTCATCGGCCGCCAGTGCAACCGCTGCG  
Sbjct: 38400 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGGCGTCATCGGCCGCCAGTGCAACCGCTGCG 38459

Query: 409 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 447  
ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG  
Sbjct: 38460 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 38498

FIG. 4

Score = 1000 (352.0 bits), Expect = 2.4e-98, P = 2.4e-98  
Identities = 162/186 (87%), Positives = 172/186 (92%), Frame = +3

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Query:      3 YLGINCVDACHLNPCENMGACVRSPGSPQGYVCECGPSHYGPYCENKLDLPCPRGWGWP 182
              Y G  CVDAC LNPC+++ ACVRSP +P+GY CECGP HYG YCENK+DLPCP+GWWGWP
Sbjct: 1917 YFGKKCVDACLLNPCKHVAACVRSPNPPRGYSCECGPGHYGQYCENKVDLPCPKGWWGWP 1976

Query:     183 VCGPCHCAVSKGFDPCNKTNNGQCQCKENYYKLLAQDTCLPCDCFPFHGSHSRTCDNATGQ 362
              VCGPCHCAVS+GFDPCNKTNNGQCQCKENYYK AQD CLPCDCFPFHGSHSR CDM TCQ
Sbjct: 1977 VCGPCHCAVSQGFDPDCNKTNNGQCQCKENYYKPPAQDACLPDCFPFHGSHSRACDMDTGQ 2036

Query:      61 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCAGTCACT 120
              |||
Sbjct: 33445 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCAGTCACT 33504

Query:     121 ACGGGCCGTACTGTGAGAACAA 142
              |||
Sbjct: 33505 ACGGGCCGTACTGTGAGAACAA 33526

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FIG. 5

Score = 12924 (4549.5 bits), Expect = 0.0, P = 0.0  
Identities = 2451/3034 (80%). Positives = 2677/3034 (88%)

Query: 1 MAPPPFPVLPVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPGCTYAVGAAC TFR- 59  
MAP P VLP L+LLAAAA LPA+ L AAWE RVPGG RAFAL PG +Y + TFR

Sbjct: 1 MAPSSPRVLPALVLLAAAA-LPALELGAAWELRVPGGARAFALGPGWSYRLDTTRTFRE 59

Query: 60 ---APRELLDVGRD-GRLAGRRRVSG-AGRPLPLQVRLVARSAPTALSRRRLRARTHLPGC 114  
RE GR G AG + AGR LPLQVRLVAR APTA S LRAR + C

Sbjct: 60 LLDVSREGPAAGRRLGLGAGTLGCARLAGRLPLQVRLVARGAPTAPSLVLRARAYGARC 119

Query: 115 GARA-RLCGTGARL-----CG-ALCFVPGGCAAAQKSALAAPTTL PACRCPPRP 162  
Q R R GA L G ALCFP GG AA+ S L A T PAC CPP

Sbjct: 120 QVRLRLRSARGAELRSPAVRSVPGLGDALCFPAAGGGAASLTSVLEAITNFPACSCPPVA 179

Query: 163 RPRCPGRPICLP PPGSVRLRLCALRRAAGAVRVGLALEAATAGTPSASPSPPPLPNL 222  
C PICL PGGS LRL+CAL RAAGAV V L ++A T+OTPS SPS SP L NL

Sbjct: 180 GTGCRRGPICLRPGGS AELRLVLCALGRAAGAVWVELVQA-TSGTPSESFSVSPSLL-NL 237

Query: 223 PEARAGPARRARRGTSGRQSLKFPMPNYQVLFENEPAGTILILQLHAHYTIEGEEERVS Y 282  
+ RAG RR+RRCT S +FP+P+YQV++ ENEPAGT +++L AH EG+ R+SY

Sbjct: 238 SQPRAGVVRSSRRGTGSSTSPQFPLPSYQVSVPENEPAGTAVIELRAHDPDEGDAGRLSY 297

Query: 283 YMBGLFDESRGYFRIDSATGAVSTDSVLDRETKETHVLRVKAVDYSTPFRSATTYITVL 342  
ME LFDERS GYF ID+ATGAV+T LDRETK+THVL+V AVD+ +P RSA TY+TV

Sbjct: 298 QMEALFDESRNGYFLIDAATGAVTTARS LDRETKDTHVLKVS AVDHGSPRRSAATYLTVT 357

Query: 343 VKDTNDHSPVFEQSEYREVRVRENLEVGVEVLTIRASDRSPINANLRYRVLGGAWDV FQL 402  
V DTNDHSPVFEQSEYRER+RENLEVGVEVLTIRA+D D+P NAN+RYR+L GA VF++

Sbjct: 358 VSDTNDHSPVFEQSEYRERIRENLEVGVEVLTIRATDGDAPSNNMRYALLEGAGGVFEI 417

Query: 403 NESSCVVSTRAVLDR EEA EYQLLVEANDQGRNPGPLSATATVYIEVEDENDNYPQFSEQ 462  
+ SGVV TRAV+DRE EAEYQLLVEANDQGRNPGPLSA+ATV+I VEDENDNYPQFSE+

Sbjct: 418 DARS GVVTRAVVDRE EAEYQLLVEANDQGRNPGPLSASATVHIVVEDENDNYPQFSEK 477

Query: 463 NYVVQVPEDVGLNTAVLRVQATDRDQGNAAIHYSILSGNVAGQFYLHSLSGILDVINPL 522  
YVVQVPEDV +NTAVLRVQATDRDQGNAAIHYSI+SGN+ GQFYLHSLSG LDVINPL

Sbjct: 478 RYVVQVPEDVAVNTAVLRVQATDRDQGNAAIHYSIVSGNLKGQFYLHSLSGSLDVINPL 537

Query: 523 DFE DVQKYSLSIKAQDGRPPLINSSGVSVQVLDVNDNEPIFVSSPPQATVLENVPLGY 582  
DFE +++Y+L IKAQDGRPPLINSSG+VSVQVLDVNDN PIFVSSPPQA VLENVPLG+

Sbjct: 538 DFEAIREYTLRIKAQDGRPPLINSSQLVSVQVLDVNDNAPIFVSSPPQA AVLNVPLGH 597

Query: 583 PVVHIQAVDADSGENARLHYRLVDTASTTLGGGSAGPKNPAPTDFPFQIHNSSGNITVC 642  
V+HIQAVDAD+GENARL YRLVDTAST +GG S +NPA PDFPFQIHNSSGNITVC

Sbjct: 598 SVLHIQAVDADAGENARLQYRLVDTASTIVGSSVDSNPASAPDFPFQIHNSSGNITVC 657

Query: 643 AELDREEVEHYSGVEAVDHGSPMSSSTSVSITVLDVNDNDPVFTQPTYELRLNEDAAV 702  
AELDREEVEHYSGVEAVDHGSP M888 SVSITVLDVNDNDP+FTQP YELRLNEDAAV

Sbjct: 658 AELDREEVEHYSGVEAVDHGSPAMSSSASVSITVLDVNDNDPMFTQPFVYELRLNEDAAV 717

Query: 703 GSSVLTLOARDRDANSVITYQLTGGNTRNRFALSSQGGGLITLALPLDYKQEQQYVLAV 762  
GSSVLT/L+ARDRDANSVITYQLTGGNTRNRFALSSQ GGGGLITLALPLDYKQE+QYVLAV

Sbjct: 718 GSSVLT/LRARDRDANSVITYQLTGGNTRNRFALSSQSGGLITLALPLDYKQERQYVLAV 777

Query: 763 TASDGTASHTAHVLINVT DANTHRPFVQSSHYTVSVSEDRPVGTSIATLSANEDTGENA 822  
TASDGTASHTA V INVT DANTHRPFVQSSHYTVSVSEDRPVGTSIAT+SA DEDTGENA

Sbjct: 778 TASDGTASHTAQVF INVT DANTHRPFVQSSHYTVSVSEDRPVGTSIATISATD EDTGENA 837

Query: 823 RITYVTQDPVPQFRIDPDSGTYMTMELDYENQVAYTLTMAQDNQIPQKSDTTTLEILI 882  
RITYV++DPVPQFRIDPD+GT+YTM EL DYE+Q AYTL I AQDNQIPQKSDTT+LEILI

Sbjct: 838 RITYVLEDVPVPQFRIDPDGTGTIYTMELDYEDQAAYTLAITAQDNQIPQKSDTTSLLEILI 897

# FIG. 5 Continued

Query: 883 LDANDNAPQFLWDFYQGSIFEDAPPSTSIQVSATDRDSGPNGRLLYTFQGGDDGDDGY 942  
 LDANDNAP+FL DFYQGS+FEDAPPSTS+LQVSATDRDSGPNGRLLYTFQGGDDGDDGY  
 Sbjct: 898 LDANDNAPRFLRDFYQGSVPEDAPPSTSVLQVSATDRDSGPNGRLLYTFQGGDDGDDGY 957

Query: 943 IEPTSGVIRTQRRLDRENAVYNLWALAVDRGSPPLSASVEIQVTILDINDNAPMFEKD 1002  
 IEPTSGVIRTQRRLDRENAVYNLWALAVDRGSP PLSASV IQV++LDINDN P+FEKD  
 Sbjct: 958 IEPTSGVIRTQRRLDRENAVYNLWALAVDRGSPNPLSASVGIQVSULDINDNPFVFEKD 1017

Query: 1003 ELLEFVEENNPFVGSVVAKIRANDPDEGPNQIMYQIVEGDMRHFFQLDLLNGDLRAMVEL 1062  
 ELLEFVEEN+PVGSVVA+IRANDPDEGPNQI+YQIVEG++ FQLDLL+GDLRA+VEL  
 Sbjct: 1018 ELLEFVEENSPVGSVVARIRANDPDEGPNQIYQIVEGNVPEVFQLDLLSGDLRALVEL 1077

Query: 1063 DFEVRREYVLVVQATSAPLVSRAVHILLVDQNDNPFVLPDFQILFNMYVTNKSNSFPTG 1122  
 DFEVRR+Y+LVVQATSAPLVSRAVHI L+QNDNPF LPDFQILFNMYVTNKSNSFP+G  
 Sbjct: 1078 DFEVRDYMLVVQATSAPLVSRAVHIRLLDQNDNPFELPDFQILFNMYVTNKSNSFPPSG 1137

Query: 1123 VIGCIPAHDPDVSLSNYTFVQGNELRLLLDPATGELQLSRDLNNRPLEALMEVSVSD 1182  
 VIG IPAHDPD+SDLSNYTF+QGNEL LLLDPATGELQLSRDLNNRPLEALMEVSVSD  
 Sbjct: 1138 VIGRIPAHDPDLSDLSNYTFVQGNELSLLLDPATGELQLSRDLNNRPLEALMEVSVSD 1197

Query: 1183 GIHSVTAFCTLRVTIITDDMLTNSITVRLNMSQEKFLSPLLALFVEGVA AVLSTTKDDV 1242  
 GIHSVTA CTLRVTIITDDMLTNSITVRLNMSQEKFLSPLL+LFVEGVA VLSTTKDD+  
 Sbjct: 1198 GIHSVTALCTLRVTIITDDMLTNSITVRLNMSQEKFLSPLLALFVEGVATVLSTTKDDI 1257

Query: 1243 FVFNQNDTDVSSNINLVTFSSALLPGGVRGQFPSEDLQEIQYILNRTLLTTISTQRLPFP 1302  
 FVFN+QNDTDVSSNINLVTFSSALLPGG RQ+FPSEDLQEIQYILNRTLLTTIS QRLPFP  
 Sbjct: 1258 FVFNQNDTDVSSNINLVTFSSALLPGGTRGRFPSEDLQEIQYILNRTLLTTISAQRLPFP 1317

Query: 1303 DDNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHPINGLRRCRCPGFTGDCYET 1362  
 DDNICLREPCENYMKCVSVLRFDSSAPF+SSTTVLFRPIHPI GLRCRCPPGFTGDCYET  
 Sbjct: 1318 DDNICLREPCENYMKCVSVLRFDSSAPFISSTTVLFRPIHPITGLRCRCPPGFTGDCYET 1377

Query: 1363 EIDLCSYDPCGANGRCRSREGGYTCECFEDFTGEHCVDARSGRCAAGVCCKNGGTCVNLL 1422  
 EIDLCSY+PCGANGRCRSREGGYTCECFEDFTGEHC+V+ RSGRCA+GVCKNGGTCVNLL  
 Sbjct: 1378 EIDLCSYDPCGANGRCRSREGGYTCECFEDFTGEHCQVNVRSGRCASGVCKNGGTCVNLL 1437

Query: 1423 IGGFHCVCPPGEYERPYCEVTTRSFPPQSFVTFRGLRQRFHFTISLTFATQERNGLLLYN 1482  
 IGGFHCVCPPGEYE PYCEV+TRSFPPQSFVTFRGLRQRFHFT+SL FATQ+RN LLLYN  
 Sbjct: 1438 IGGFHCVCPPGEYEHFYCEVSTRSFPPQSFVTFRGLRQRFHFTVSLAFATQDRNALLYN 1497

Query: 1483 GRFNEKHDFIALBIVDEQVQLTFSAGETTTTVA PKVPSGVSDGRWHSVQVQYNNKPNIGH 1542  
 GRFNEKHDFIALBIV+BQ+QLTFSAGETTTTV P+VP GVSDGRWHSV VQYNNKPNIGH  
 Sbjct: 1498 GRFNEKHDFIALBIVEBQLQLTFSAGETTTTVPQVPGGVSDGRWHSVQVQYNNKPNIGH 1557

Query: 1543 LGLPHGPSGEKMAVVTVDCCDTMAVRFGKDIGNYSCAAQGTQTSKKSLLDTGPLLLGG 1602  
 LGLPHGPSGEK+AVVTVDCCD +AV FG +GNYSCAAQGTQ+GSKKSLLDTGPLLLGG  
 Sbjct: 1558 LGLPHGPSGEKVAVVTVDCCDAVAVHFGSYVGNYSCAAQGTQSGSKKSLLDTGPLLLGG 1617

Query: 1603 VPNLPEDFPVHNRQFVGCNRNLSVDGKNVDMAGFIANNGTREGCAARRNFCDGRRCCQNGG 1662  
 VPNLPEDFPVH+RQFVGCNRNLS+DG+ VDMA FIANNGTREGCAARRNFCDGRRCCQNGG  
 Sbjct: 1618 VPNLPEDFPVHSRQFVGCNRNLSIDGRIVDMAAFIANNGTREGCASQRNFCDCGTCQNGG 1677

Query: 1663 TCVRNRMNYLCECLRPFGGKNCEQAMPHPQLFSGESVSVWSDLNIIISVPWYLGIMFRTR 1722  
 TCVRNRM NYLCECLRPFGGKNCEQAMPHPQ P+GESVW WSDL+I ISVPWYLGIMFRTR  
 Sbjct: 1678 TCVRNRMNYLCECLRPFGGKNCEQAMPHPQRFTGESVSVWSDLNIIISVPWYLGIMFRTR 1737



# FIG. 5 Continued

Query: 2563 VRNIDTGPMRFYVVGWGIPAIVTGLAVGLDPQGYGNPDFCWLSQLQDTLIWSFAGPIGAV 2622  
VRNIDTGPMRFY+VVGWGIPAIVTGLAVGLDPQGYGNPDFCWLSQLQDTLIWSFAGP+G V

Sbjct: 2578 VRNIDTGPMRFYHVVGWGIPAIVTGLAVGLDPQGYGNPDFCWLSQLQDTLIWSFAGFVGTV 2637

Query: 2623 IIINTVTSVLSAKVSCQRKHYYGKKGIVSILLRTAFLLLLISATWLLGLLAVNRDALSF 2682  
IIINTV VLSAKVSCQRKHYY +KG+VS+LRTAFLLLL++ATWLLGLLAVN D LSF

Sbjct: 2638 IIINTVIFVLSAKVSCQRKHYYERKGVVSMRLTAFLLLLVTATWLLGLLAVNSDTLSF 2697

Query: 2683 HYLFAIFSGLQGPVLLFHCVLNQEVKHLKGVLCGRKLHLED SATTRATLLTRSLNCNT 2742  
HYLFA FS LQC FVLLFHCV ++EVRKHL+ VL G+KL L+DSATTRATLLTRSLNCN

Sbjct: 2698 HYLFAAFSCLQGIFVLLFHCVAHREVRKHLRAVLAGKKQLDSDSATTRATLLTRSLNCNN 2757

Query: 2743 TFGDGPDMRLRTDLGESTASLDSIVRDEGIQKLGVSGLVRGSHGEPDASLMPSRCKDPFG 2802  
T+ +GPDMLRT LGESTASLDS RDEG+QKL VSSG RG+HGEPD S +PR+ K G

Sbjct: 2758 TYSEGPDMLRTALGESTASLDSTTRDEGVQKLSVSSGPARGNHGEPDTSFIPRNSKKANG 2817

Query: 2803 HDSDSDSELSDLDEQSSSYASSHSSDSEDDGVGAZEKWDPARQAVHSTPKGDAVANHVPA 2862  
DSDSDSELSDLDE SSSYASSH+SDSEDDG AE+KW+PA G HSTPK DA+ANHVPA

Sbjct: 2818 PDSDSDSELSDLDEHSSSYASSHTSDSEDDGGEAEDKWNPAAGPAHSTPKADALANHVPA 2877

Query: 2863 WPDQSLAESDSEDPSGKPRKLVETKVSVELHREEQCSHRGEYPPDQESGGAAR---LASS 2919  
WPD+SLA SDSE+ +P LKVETKVSVELHR+ QG+H G+ P D ESG A+ + SS

Sbjct: 2878 WPDESLAGSDSEELDTEPHLKVETKVSVELHRQAQGNHCQDRPSPESGVLAQFVAVLSS 2937

Query: 2920 QPPEQRKGILKNKVITYPPPLTLTEQTLKGRRLREKLADCEQSPTSSRTSSLGSG----GPD 2975  
QP EQRKQILKNKVITYPPPL EQ LK RLREKLADCEQSPTSSRTSSLGSG D

Sbjct: 2938 QPQEQRKQILKNKVITYPPPLP--EQPLKSLRLREKLADCEQSPTSSRTSSLGSGDGVHATD 2993

Query: 2976 CAITVKSPPGREPGRDHLNGVAMNVRTGSAQADGSDSEKP 3014  
C IT+K+P REPGR+HLNGVAMNVRTGSAQA+GSDSEKP

Sbjct: 2996 CVITIKTPRREPGRHLNGVAMNVRTGSAQANGSDSEKP 3034





**FIG. 6 Continued**

[illegible]

FIG. 7

TGGAGTTTGTGCGGGCGCTGTGGCTGGGCCTGGCGCTGCCGCTGGGGCCGGGGTCCCGGGGGGC  
 ACCCTCAGCCGTGCGGGGTCTTGGCGCGCTCGGGGGCTCCGTGCCCTGGCGCGCCCTCTGCCCC  
 CGCGCCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCCGCCCTGGCGCGCGGGCTGCC  
 CACAACCTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCCGGACCCCGCCTCGCTGACCCCG  
 GCCTGTGCCAGGCGCTGGTGCCTCCGGGGCTGGCGGCCCTGCTCCCTTTCCCGAGGCTCGGCCCG  
 GCTGCTGCAGCTGCACTTCCTGGCGGGCGGCCACCGAGAACCCCGTCTCAGCCTGCTGCGGGCGG  
 GCGCGCGCGCCCCCTCGGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG  
 GACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGAGCTCGGCCTGGCCC  
 GTGCCGCACTCAGGACCCCGCGCGCTGGTGGCCCTCTGGACAAGCCGGGGCTGGCCGGCCCCCAC  
 GCTGGTCTGGAACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCCGGCACCCCTGGCCCCGA  
 GCGCGGCCAGTGGGGGGTGAAGCACCGGTACCCGCGGGCGTCCCTCCTCGCTGTGACATCGCCC  
 TGCCCGTCCGGTGTGGAGGCCGTACCTCCCGGCCCCCACTGGCTGTTGGGGACACCACTGCCGCG  
 AAGGCCCTGCCACCCGCGGGCTGCCACAGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCC  
 CTGGAGGCCCGCATCCATGACATTGTGCAACTGGTGGCCCGCGCTGGGCACTGCGGCCAGGT  
 CAGCGGAAGCGAGCCCTCCTCCCGCCCCGGTCAACTGCCGGACCTGCAGCCGGCGGGGCCCGA  
 TCCCCGGGGCGCTTCTTGGCACGGTTCCTGGCCAACACGTCTTCCAGGGCGGCAAGGGCCCCGTG  
 JGGTGACAGGCAGCTCCCCAGACGAAGACGGGAGTGCCAGCGGGGAGCTGTGCCCTGGACCT  
 GCACCAACGACTCGGCCACCTGGACGCACTGTTGCCGCGCTGGCCAACGGCTCAGCGCCCCGT  
 CCCTGCGCAAGTGTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCC  
 TCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGOCTGGGGACGGCCGCTGGACC  
 GCCTGGTCCGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTCAACAGCTTCAGTATCAACTCC  
 CCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCAACAGCCTGGGCATCATGGTGGGG  
 ACGGGACACGGCTCACCCATCGGTGCTTTATGTGGCCCTGCACTGGTCCACGTGGTGGGGT  
 TTTGGGGCCCTGCACCTCAACGCGCTCTTCTCTACCGGTGTACGAGTGGCGTAGCCCCACGGCCT  
 CGCCAGTGGCGGCAACCGCAGCACCGTCTTCTCTCTCTCAGCCCTCAACCTGTGCTACGCCA  
 TCTCTTACAGCGCACCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGGCCGCTGCTCATGAACCT  
 TGGGCCATCTTCTGCCCTGCTGGTGTGCTGCTCAGCTACACGGCCAACCTGGCTCCCGTCATGGTGGG  
 ACAAGACCTTCGAGGAGCTGTCCGGGATCCACGAACCCCAAGGGCTTCCGCTTCGGCACCGTGTGG  
 AGAGCAGCGCGAGGCGTACATCAAGAAGAGCTTCCCGACATGCACGCACACATCGCGCGCAC  
 JCGCGCCACCAAGCCCCGCGCGCTCGCCATGCTCAAGAGCGAACCCCCCAAGCTCAACGCCCTTC  
 CATGGACAAAGTGGCTCTGGACTACGAGGTCTCATGGACGCGGACTGCAAACTGCTGACCGTGG  
 AAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCGAGAACTCGCCCTCACTCCAACT  
 TCCGAGTTTCATCAGCCGCTACAACTCCTCCGCTTCATCGACCTGCTCCACGACAAGTGGTACAAG  
 TGGTGCTTGGCGCAAGCGGGTCTTTGCGGTTACAGAGACCTGCAGATGAGCATCTAACCTTCG  
 JGGCTCTTGGTGTGCTGTGCTGGCCCTGGGAGCGCTCTGCTCAGCTCGCTGGGCGAGCACGC  
 TCTTCCGCTTGGCGCTGGCGCGCATCCCAAGGGGAGCAGGCTGCACTACTGGCTGCACACAGC  
 GAAAATCCACCGCGCCCTCAACACGGAGCCAACAGAGGGGTGGAAGGAGGAGACGGCAGAGGC  
 JAGGCCAGCGGCCCGGAGGTGGAGCAGCAGCAGCAGCAGGACCAAGGCTCCGGAGG  
 TGGAAACGGGGCGCGCCGGGCCGTGGACAAGGAGCGCGCGTGGCGTTCTTGTGAGGCGCGCG  
 GTTGTGGCAACCGAAGCGGACGCGGAGGCGGAGGCTGGCCCGGAGAGGGCCCCGTCTGGCTGT  
 TCTACGGCCGCGCGCCCGCCCAAGGCCACGGGGCCCCCAGCCCGGGGAGCTGCAGGAGC  
 GAGCGCCCATCGAAGTCGCGCGTGAGCGCTCCGACAGGCCCTGGTGGCGCGCGGCCAGCTCC  
 GCACAGCTCGGGGACAGCGCACGTACCGGCTCGGGCTTGCTTCAAGCCAGAGCGCCCCCG  
 GAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 8

IEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRI  
LSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL  
SILRREARAPGAPNFFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALC  
RTQDPGGLVALWTSRAGRPPQLVLDLSRDTGDAGLRARLAPMAAPVGG  
EAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLFPKALFTAGLP  
QLLALGEVARPFLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCODLQ  
PAGFESPGRFLARFLANTFQGRTPGVWVTGSSPDEDGQCPAGQLCLDPGT  
NDSATLDALFAALANGSAPRALRKCCYGYCIDLLERAEDTPDFELYL  
VGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS  
PFFSTSLGITVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLT  
VYEWRSPLYGLTPRGRNRSTVFSYSSALNLCAILFRRTVSSKTPK  
CPTGRLLMNLWAFCLLVLSSTANLAAMVVGDKTFEELSGIHD  
PKGFRFOTVWE SAEAYIKKSFPDMHAHMRRHSAPTTPROVAM  
LTSDFPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFJEGY  
GIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCG  
KRVPAVTETLQMSIYHFAGLFVLLCGLGSALLSSLGEHAFF  
RLALPRIRKGSRLQYWLHTSQKIHRALNTEPFGSKEETA  
EAEPSQPEVEQQQIQDQPTAPEGWKRARRAVDKERRVRFL  
LEPAVVVAPEADAEAEAAPREGPVWLCSYGRPPAARFTGAP  
PGELQELERRIEVARERLRQALVRRGQLLAQLQDSARHR  
PRLLQARAAPAEAPPHSGRPGSQE

FIG. 9

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(5) = 0.0  
Identities = 928/1076 (86%), Positives = 928/1076 (86%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGCGGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847  
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G  
Sbjct: 22736 CCCTGCC-CCTAGGTTCCCTGGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCCGTGTG 22792

Query: 848 AGGTGGCAG-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901  
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G  
Sbjct: 22793 -GGTGACAGGCAGTCC-CAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCGGCCCG 960  
CC GG C C GGG G C G CC GG CA C G G AGC C C GCC G  
Sbjct: 22850 CCGGACCCACGGGGCGCCCCGGCCTGGGCCA-CGGTGGGCAGCTGGCGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGACCTGCAGCCGGCGGGCCCGAGTCCCCGGGGCG-CTTCTTGGCACG 1019  
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G  
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTGCCCTGTCAGC-GCCCCCGCCCCACAGGGTGCCCG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCTTCCAGGGCCGCACGGGC-CCCGTGTGGGTGACAGGCA 1075  
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C  
Sbjct: 22965 GT--CTGGCCCAAGCTGCGTG-TGGTAACGCTGTTGGAACACCCATTTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAAGTGCAGCGGGGAGCTGTGCCTGGACCCCTGGCACCA 1135  
G CCAGACGAAGACGGGCAAGTGCAGCGGGGAGCTGTGCCTGGACCCCTGGCACCA  
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAAGTGCAGCGGGGAGCTGTGCCTGGACCCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCTGGACGCACTGTTTCGCCCGCTGGCCAACGGCTCAGCGCCCCGTG 1195  
ACGACTCGGCCACCTGGACGCACTGTTTCGCCCGCTGGCCAACGGCTCAGCGCCCCGTG  
Sbjct: 23080 ACGACTCGGCCACCTGGACGCACTGTTTCGCCCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255  
CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA  
Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 1315  
CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG  
Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 23259

Query: 1316 GCGCCTGGACCGGCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCACATGGCGGTACCA 1375  
GCGCCTGGACCGGCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCACATGGCGGTACCA  
Sbjct: 23260 GCGCCTGGACCGGCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 1435  
GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA  
Sbjct: 23320 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGGGGCACGGGACACGGCCTCACCCATCGGTGCCTTTATGT 1495  
CCAGCCTGGGCATCATGGTGGGGCACGGGACACGGCCTCACCCATCGGTGCCTTTATGT  
Sbjct: 23380 CCAGCCTGGGCATCATGGTGGGGCACGGGACACGGCCTCACCCATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACCGCGCTCT 1555  
GGCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACCGCGCTCT

# FIG. 9 Continued

Sbjct: 23440 GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 1615  
TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA

Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 1675  
GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA

Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCCCTGCTCATGAACCTCTGGGCCA 1735  
CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCCCTGCTCATGAACCTCTGGGCCA

Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCCCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTTCATGGTCGGGG 1795  
TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTTCATGGTCGGGG

Sbjct: 23680 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTTCATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTCTGGGGATCCACGACCCCAAGGGCTTCCGCTTCGGCACCG 1855  
ACAAGACCTTCGAGGAGCTGTCTGGGGATCCACGACCCCAAGG C GC TCGG

Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTCTGGGGATCCACGACCCCAAGGTGGGCGGCCTCGGGGGG 23799

Query: 1856 TGTGGGAG 1863  
TG GGG G

Sbjct: 23800 TGGGGGTG 23807



FIG. 10

Score = 2426 (854.0 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 463/474 (97%), Positives = 464/474 (97%), Frame = +1

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Query:  1063 WVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
          +V   PDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct:  427 FVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query:  1243 LAEDTPPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
          LAEDTPPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct:  487 LAEDTPPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query:  1423 PFFSTSLGIMVRARDTASPIGAFMNPLHNSWTLGVFAALHLTALFLTVEYWRSPYGLTPR 1602
          PFFSTSLGIMVRARDTASPIGAFMNPLHNSWTLGVFAALHLTALFLTVEYWRSPYGLTPR
Sbjct:  547 PFFSTSLGIMVRARDTASPIGAFMNPLHNSWTLGVFAALHLTALFLTVEYWRSPYGLTPR 606

Query:  1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCTGRLLMNLWAI FCLLVLSSTYANLAA 1782
          GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCTGRLLMNLWAI FCLLVLSSTYANLAA
Sbjct:  607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCTGRLLMNLWAI FCLLVLSSTYANLAA 666

Query:  1783 VMVGDKTFEELSGIHDPK-----CFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 1944
          VMVGDKTFEELSGIHDPK          CFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP
Sbjct:  667 VMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 726

Query:  1945 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFATIEGYGIGLPQNSPLTSN 2124
          RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFATIEGYGIGLPQNSPLTSN
Sbjct:  727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFATIEGYGIGLPQNSPLTSN 786

Query:  2125 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2304
          LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct:  787 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query:  2305 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 2466
          LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP
Sbjct:  847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 900

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FIG. 12

ATGAGAGTTTGTGCGGGCGCTGTGGCTGGCCCTGGCCCTGGCCCTGGGGCCGGGCTCCGCGGGGGGC  
CAOCCCTCAGCCGTGCGGCGTCTTGGCGCGCCTCGGGGCTCCGTGCGCTGGGCGCCCTCCTGCCCC  
GCGCGCTCTGCGCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCGCCCTGGCGCCGCGGCTGCC  
GCACAACCTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCCGCGAACCCCGCTCGCTGACCCGG  
GGCTGTGCCAGGCCGTGGTGGCTCCGGGCGTGGCGGCCCTGCTCGCTTTCCCGAGGCTCGGCCCG  
AGCTGCTGCAGCTGCACTTCTGGCGGCGGCCACCGAGAACCCCGTGTCTCAGCTGCTGCGGCGGG  
AGGCGCGCGCGCCCTCGAGGCCCGGAACCCATTCCACCTGCACTGCACTGGGCCAGCCCCCTGG  
AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGACGTGGGCTGGGCC  
TGTGCCGCACTCAGAACCCCGGCGGCTGGTGGCCCTCTGGAACAAGCCGGGCTGGCGGGCCCCAC  
AGCTGGTCTTGAACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGGGGGCAAGCCTGGCCCCGA  
TGGCGCGCCAGTGCGGGGTGAAGCACCGGTACCGCGGGCGTCTCTCTCGGCTGTGACATCGCCC  
GTGCCCCCTCGGCTGTGAGGCCGTACCTCCCGGCCCGCCACTGGCTGTTGGGAGACCACTGCCGCC  
CAAGGCCCTGCCACCGCGGGGTGCCACCAAGGCTGCTGGCGCTGGGCGAGTGGGACGAAACCC  
GCTGGAGGCGCCATCCATGACATTGTGCAACTGGTGGCCCGGGCTGGGCAATGGCGCCAGGT  
GCAGCCGAAGCGAGCCCTCTCCCCGCCCCGTTCAACTGCGGGGAACTGCAGCCGCGCGGGCCCCGA  
GTCCCCGGGGCGCTTCTTGGCACGGTCTCTGGCCAACAAGTCTTCCAGGGCCGCAAGGGCCCCGTG  
TGGGTGACAGGCAAGCTCCCCAGACGAAGACGGGCAAGTGGCCAGCGGGGCAAGCTGTGCTTGAACCT  
GGCAACAACGACTCGGCCAACCTGGACGCACTGTTGCGCGCGCTGGCCAACGGCTCAGCGCCCCGT  
GCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCC  
TTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGCGGCCCTGCGGGAAGCGCGCTGGACC  
GGCTGGTTCGGGGAACTGCTGGCCGGCGGGGCCCAATGGCGGTCAACGACTTCAATATCAACTCC  
GCCCGCTCAACAGTGGTGGACTTCAACAGCCCCCTTCTTCTCCACCAGCTGGGCATCATGGTGGGG  
CAGGGGACAGGGCTCACCCATCGGTGCTTTATGTGCCCCCTGCACTGGTCCACGTGGCTGGGCGT  
CTTGGGGCCCTGCACTCACCGCGCTCTTCTCAACGTGTACGAGTGCCGTAGCCCCTAGGGCTC  
ACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCTCAGCCCTCAACCTGTGCTACGCCA  
TCTCTTCAGACGACCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCT  
TGGGGCATCTTCTGCTGCTGGTGGTGTCCAGCTACACGGGCAACCTGGCTGCCGTATGGTGGG  
TACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGCTGCACCACCGGCGCGAGGGCTT  
TGGCTTCGGCACCGTGTGGGAGAGCAGGGCCGAGCGGTACATCAAGAAGAGCTTCCCCGACATGCA  
TGCACACATGGGGGCCACAGCGGCCCAACAGGCCCGCGGCGTGGCATGCTCAGAGCGAACCC  
TCCCAAGCTCAACGCTTCATCATGGACAAGTGGCTCTGGACTAAGAGGTCTCATCGACGCCGAC  
TGCAAACCTGCTGAACGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCCAGAAC  
TGGCGCTCACTCCAAOCTGTCCGAGTTCATCAGCCGCTACAAATCTCTCGGCTTCATCGACCTGCT  
TACGACAAGTGGTACAAGATGGTGGCTTGGGCAAGCGGGTCTTTGGGTTACAGAGAACCTGCA  
TATGAGCATCTACCACTTCGCGGGGCTCTTGGTGTGTGCTGTGCTGGCCCTGGGCAAGGCTCTGCTC  
TCTGCTGGGCGAGCACGCTTCTTCCGCTGGCGCTGGCGCGCATCGCAAGGGGAGCAGGCTG  
TAGTACTGGCTGCACCAAGCCAGAAAATCCACCGCGCCCTCAACACGGAGGACACAGAGGGGTG  
TAGGAGGAGACGGCAGAGGCCGAGGCCAGCGGCCCGAGGTGGAGCAGCAGCAGCAGCAGG  
TCCAGCCAAACGGCTCCGAGGCGTGGAAAACGGGCGCGCCGGGCCGTGGACAAGGAGCGCGCGT  
TCTTCTGTGGAGCCCGCGGTGGTGTGGCAACCGAAGCGGACGCGGAGGCGGAGGCTGGCGG  
TGAAGGGGCCCGTCTGCTGTGCTCTACGGCGCCCGCGCGCAAGGCCACCGGGGGCCCC  
TACCCCGGGAGCTGCAGGAGCTGGAGCGCGCATCGAAGTGGCGGTGACGGCTCCGCCAGGC  
TGGTGGGCGCGGCCAGCTCTGGCACAGCTCGGGGACGCGCAGTCAACCGCTCGCGCTT  
TTCAGGCCAGAGCGGCCCGCGGAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 13

MEFVRALWLQLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH  
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVLSSLRREARAP  
LGAPNPFHLQLHWASPLETLDDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS  
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP  
POLLALGEVARPPLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCGLQAPAGPESPGRFLARFLANT  
SFQGRTPGVVWVGSSPDDEGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER  
LAEDTPFDLFLYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSPSINSARSQVVDFTSPFPSTSLGI  
MVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYEWRSPLYOLTTPRGRNRSTVESYSSALNLC  
YAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSSTANLAAMVVGDKTFEELSGIHDPKLHHPAQGFR  
FGTVWESSAEAYIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAMDKSLLDYEVSIDADCKLL  
TVGKPFIEGYGIQLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVFAVTETLQMSIYHFAQ  
LFVLLCLGLGSALLSSLGHHAFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEPSGPE  
VEQQQQQQDQPTAPEGWKRARRAVDKERRVRFLLEPAVVVAPEADAEAEAAPREGPVWLCSYGRPPA  
ARPTGAPOPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSGRPGS  
QE

FIG. 14

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(3) = 0.0  
Identities = 948/1107 (85%), Positives = 948/1107 (85%), Strand = Plus / Plus

Query: 788 CACTGCGCCCAAGGCCCTGCCACCGCGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847  
C CTGCC CC A G C CTG CCA C CG CT CCA GC C GGC C G G G  
Sbjct: 22736 CCTGCC-CCTAGGTTCTTCCGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCGCTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901  
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G  
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACTTTAAGGTGTGGAGCCT-TGG 22849

Query: 902 CCGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCCG 960  
CC GG C C GCG G C G CC GG CA C G G AGC C C GCG G  
Sbjct: 22850 CCGGACCCACGGGGCGCCCGGCTGGGCCA-CGGTGGGCAGCTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGGACCTGCAGCCGGCCGGGCGGAGTCCCCGGGGCG-CTTCTTGGCAGC 1019  
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G  
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTCCCTCTGCACG-GCCCCCGCCCCACAGGGTGGCCAG 22964

Query: 1020 GTTCTGGCC-AA-CA-CGTCTTCAGGGCCGCAAGGGC-CCCGTGTGGGTGACAGGCA 1075  
GT CTGCC AA C CGT T A GC G G C CCC T TG GT G C  
Sbjct: 22963 GT--CTGGCCCAAGCTGCGTG-TGTAACGCTGTTCGAACACCCATTTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAGTCCCCAGCGGGCAGCTGTGCTTGGACCCTGGCACCA 1135  
G CCAGACGAAGACGGGCAQTCCCCAGCGGGCAGCTGTGCTTGGACCCTGGCACCA  
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTCCCCAGCGGGCAGCTGTGCTTGGACCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCTTGGACGCACTGTTCCGCCGCTGGCCACCGGCTCAGCGCCCCGTG 1195  
ACGACTCGGCCACCTTGGACGCACTGTTCCGCCGCTGGCCACCGGCTCAGCGCCCCGTG  
Sbjct: 23080 ACGACTCGGCCACCTTGGACGCACTGTTCCGCCGCTGGCCACCGGCTCAGCGCCCCGTG 23139

# FIG. 14 Continued

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255  
 CCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA  
 Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 1315  
 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG  
 Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 23259

Query: 1316 GCCGCTGGACCGGCTGGTGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 1375  
 GCCGCTGGACCGGCTGGTGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA  
 Sbjct: 23260 GCCGCTGGACCGGCTGGTGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 1435  
 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA  
 Sbjct: 23320 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGCGGGCACGGGACACGGCCTACCCATCGGTGCCTTTATGT 1495  
 CCAGCCTGGGCATCATGGTGCGGGCACGGGACACGGCCTACCCATCGGTGCCTTTATGT  
 Sbjct: 23380 CCAGCCTGGGCATCATGGTGCGGGCACGGGACACGGCCTACCCATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 1555  
 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT  
 Sbjct: 23440 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 1615  
 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA  
 Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGGCA 1675  
 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGGCA  
 Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGGCA 23619

Query: 1676 CCGTGTCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 1735  
 CCGTGTCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA  
 Sbjct: 23620 CCGTGTCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGTGTCCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG 1795  
 TCTTCTGCCTGCTGGTGTGTCCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG  
 Sbjct: 23680 TCTTCTGCCTGCTGGTGTGTCCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGCTGCACCACC-CGGCCAG 1854  
 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAG TG C CC CGG G G  
 Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGTGGGCGGCTCGG-G-G 23796

Query: 1855 GGCTTCCGCTTCGGCACCGTGTGGGAGAGCAAGC-CGAGG 1894  
 GGCT C G T GGC G G GGG AGC G G CC GG  
 Sbjct: 23797 GGCTGCGGGT--GGCCTTGGG-GGGCTAGCGGTGGCCCCGG 23834

FIG. 15

Score = 2481 (873.4 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 469/474 (98%), Positives = 470/474 (99%), Frame = +1

```

Query: 1063 WVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
      +V      PDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct: 427 FVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
      LAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGINVRARDTASPIGAFMPLHNSTWLGVFAALHLTALFLTVEWRSFYGLTPR 1602
      PFFSTSLGINVRARDTASPIGAFMPLHNSTWLGVFAALHLTALFLTVEWRSFYGLTPR
Sbjct: 547 PFFSTSLGINVRARDTASPIGAFMPLHNSTWLGVFAALHLTALFLTVEWRSFYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA 1782
      GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPKLHHPAQGFREFGTWESSAEAYIKKSFPDMHAHMRRHSAPTTP 1962
      VMVGDKTFEELSGIHDPKLHHPAQGFREFGTWESSAEAYIKKSFPDMHAHMRRHSAPTTP
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFREFGTWESSAEAYIKKSFPDMHAHMRRHSAPTTP 726

Query: 1963 RGVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 2142
      RGVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN
Sbjct: 727 RGVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 786

Query: 2143 LSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2322
      LSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2323 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAETAEAP 2484
      LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAETAEAP
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAETAEAP 900

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24/48

[illegible]



**25/48**

[illegible]

FIG. 18

MEFVRALWLGLALALGPGSAGGHPQCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH  
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLAAATETPVLSLLRREARAP  
LGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS  
RRDTGDAGLRARLAPMAAPVCGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP  
PGLLALGEVARPPLEAAIHDIQVVARALGSAAQVQPKRALLPAPVNCGLQAPGPESPGRFLARFLANT  
SFQGRTPGVWVTGSSQVHMSRHFVWVSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQ  
VWPKLRVVTLLEHPPVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKOCYGYCI  
DLLERLAEDTPFDL FELYLVDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFFS  
TSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFTVYEWRSPLYGLTPGRNRSTVFSYSSA  
LNL CYAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSSTANLAAMVVGDKTFEELSGIHDPKLHHPA  
QGFRPGTVWESSAEAYIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDAD  
CKLLTVGKPFATIEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPCKRVFAVTETLQMSIY  
HFAGLFVLLCLGLGSALLSSLGEHAFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKERTAEAEF  
SGPEVEQQQQQQDQPTAPEGWKRARRAVDKERRVRFLEPAVVVAPEADAEAEAAAPREGPVWLCSYG  
RPPAARPTGAPQPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSG  
RPGSQE

**FIG. 19**

Score = 5188 (778.4 bits), Expect = 0.0, Sum P(4) = 0.0  
Identities = 1068/1092 (97%), Positives = 1068/1092 (97%), Strand = Plus / Plus

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Query:  1019  GGTTCCTGGCCAAACACGTCCTTCCAGGGCCGCACGGGCCCCGTTGTGGGTGACAGGCAGCT  1078
           GGTTCCTGGCCAAACACGTCCTTCCAGGGCCGCACGGGCCCCGTTGTGGGTGACAGGCAGCT
Sbjct:  22747  GGTTCCTGGCCAAACACGTCCTTCCAGGGCCGCACGGGCCCCGTTGTGGGTGACAGGCAGCT  22806

Query:  1079  CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG  1138
           CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG
Sbjct:  22807  CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG  22866

Query:  1139  CCCCCGCCCTGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACCGGGAG  1198
           CCCCCGCCCTGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACCGGGAG
Sbjct:  22867  CCCCCGCCCTGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACCGGGAG  22926

Query:  1199  GTGCCTCTGCACGGCCCCCGCCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCCGTGTGG  1258
           GTGCCTCTGCACGGCCCCCGCCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCCGTGTGG
Sbjct:  22927  GTGCCTCTGCACGGCCCCCGCCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCCGTGTGG  22986

Query:  1259  TAACGCTGTTGGAACACCCATTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC  1318
           TAACGCTGTTGGAACACCCATTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC
Sbjct:  22987  TAACGCTGTTGGAACACCCATTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC  23046

Query:  1319  CAGCGGGGCAGCTGTGCCCTGGACCCCTGGCACCAACGACTCGGCCACCCTGGACGCACTGT  1378
           CAGCGGGGCAGCTGTGCCCTGGACCCCTGGCACCAACGACTCGGCCACCCTGGACGCACTGT
Sbjct:  23047  CAGCGGGGCAGCTGTGCCCTGGACCCCTGGCACCAACGACTCGGCCACCCTGGACGCACTGT  23106

Query:  1379  TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT  1438
           TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT
Sbjct:  23107  TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT  23166

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# FIG. 19 Continued

Query: 1439 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 1498  
 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG  
 Sbjct: 23167 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 23226

Query: 1499 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCTGGTTCGGGGACC 1558  
 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCTGGTTCGGGGACC  
 Sbjct: 23227 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCTGGTTCGGGGACC 23286

Query: 1559 TGC TGGCCGGCCGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 1618  
 TGC TGGCCGGCCGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC  
 Sbjct: 23287 TGC TGGCCGGCCGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 23346

Query: 1619 AGGTGGTGGACTTCACAGCCCCCTCTTCTCCACAGCCTGGGCATCATGGTGGGGCAC 1678  
 AGGTGGTGGACTTCACAGCCCCCTCTTCTCCACAGCCTGGGCATCATGGTGGGGCAC  
 Sbjct: 23347 AGGTGGTGGACTTCACAGCCCCCTCTTCTCCACAGCCTGGGCATCATGGTGGGGCAC 23406

Query: 1679 GGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCAC TGGTCCACGTGGCTGG 1738  
 GGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCAC TGGTCCACGTGGCTGG  
 Sbjct: 23407 GGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCAC TGGTCCACGTGGCTGG 23466

Query: 1739 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACC GTGTACGAGTGGCGTAGCC 1798  
 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACC GTGTACGAGTGGCGTAGCC  
 Sbjct: 23467 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACC GTGTACGAGTGGCGTAGCC 23526

Query: 1799 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCTCTCAGCCC 1858  
 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCTCTCAGCCC  
 Sbjct: 23527 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCTCTCAGCCC 23586

Query: 1859 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 1918  
 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC  
 Sbjct: 23587 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 23646

Query: 1919 CCACGGCCCGCCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCT 1978  
 CCACGGCCCGCCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCT  
 Sbjct: 23647 CCACGGCCCGCCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCT 23706

Query: 1979 ACACGGCCAACCTGGCTGCCGTCATGGTTCGGGGACAAGACCTTCGAGGAGCTGTGGGGA 2038  
 ACACGGCCAACCTGGCTGCCGTCATGGTTCGGGGACAAGACCTTCGAGGAGCTGTGGGGA  
 Sbjct: 23707 ACACGGCCAACCTGGCTGCCGTCATGGTTCGGGGACAAGACCTTCGAGGAGCTGTGGGGA 23766

Query: 2039 TCCACGACCCCAAGCTGCACACC-CCGCGCAGGGCTTCGCTTCGGCACCGTGTGGAG 2097  
 TCCACGACCCCAAG TG C CC CGG G GGGCT C G T GGC G G GGG  
 Sbjct: 23767 TCCACGACCCCAAGGTGGCGGGCTCGG-G--GGGCTGCGGT--GGCCTTGGG-GGGCT 23820

Query: 2098 AGCAGCG-CCGAGG 2110  
 AGC G G CC GG  
 Sbjct: 23821 AGCGGTGGCCCCGG 23834

FIG. 20

Score = 4730 (1665.0 bits), Expect = 0.0, P = 0.0

Identities = 900/900 (100%), Positives = 900/900 (100%), Frame = +1

Query: 1 MEFVRAIMLGLALALGPGSAGGHPQPCGVRLRGSSVRLGALLPRAFLARARARAALARA 180  
MEFVRAIMLGLALALGPGSAGGHPQPCGVRLRGSSVRLGALLPRAFLARARARAALARA  
Sbjct: 1 MEFVRAIMLGLALALGPGSAGGHPQPCGVRLRGSSVRLGALLPRAFLARARARAALARA 60

Query: 181 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLA 360  
ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLA  
Sbjct: 61 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLA 120

Query: 361 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 540  
AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR  
Sbjct: 121 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 180

Query: 541 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 720  
TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC  
Sbjct: 181 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 240

Query: 721 DIARARRVLEAVFPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPFLAAIHDIQVLV 900  
DIARARRVLEAVFPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPFLAAIHDIQVLV  
Sbjct: 241 DIARARRVLEAVFPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPFLAAIHDIQVLV 300

Query: 901 ARALGSAAQVQPKRALLPAFVNCGDLQAGPESPGRFLARFLANTSFOGRTGPFVWVTGSS 1080  
ARALGSAAQVQPKRALLPAFVNCGDLQAGPESPGRFLARFLANTSFOGRTGPFVWVTGSS  
Sbjct: 301 ARALGSAAQVQPKRALLPAFVNCGDLQAGPESPGRFLARFLANTSFOGRTGPFVWVTGSS 360

Query: 1081 QVHMSRHFVWLSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRUV 1260  
QVHMSRHFVWLSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRUV  
Sbjct: 361 QVHMSRHFVWLSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRUV 420

Query: 1261 TLLEHPFVFARDPDEDGQCQAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 1440  
TLLEHPFVFARDPDEDGQCQAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC  
Sbjct: 421 TLLEHPFVFARDPDEDGQCQAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 480

Query: 1441 IDLLERLAEDTPFDLYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 1620  
IDLLERLAEDTPFDLYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ  
Sbjct: 481 IDLLERLAEDTPFDLYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 540

# FIG. 20 Continued

Query: 1621 VVDFTSPFFSTSLGIMVRARDTASPIGAFMPLHWSTWLGVFAALHLTALFLT/TVYENRSP 1800  
VVDFTSPFFSTSLGIMVRARDTASPIGAFMPLHWSTWLGVFAALHLTALFLT/TVYENRSP  
Sbjct: 541 VVDFTSPFFSTSLGIMVRARDTASPIGAFMPLHWSTWLGVFAALHLTALFLT/TVYENRSP 600

Query: 1801 YGLTFRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 1980  
YGLTFRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY  
Sbjct: 601 YGLTFRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 660

Query: 1981 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFFDMHAMRRH 2160  
TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFFDMHAMRRH  
Sbjct: 661 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFFDMHAMRRH 720

Query: 2161 SAPTTPRGVAM/TS DPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQN 2340  
SAPTTPRGVAM/TS DPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQN  
Sbjct: 721 SAPTTPRGVAM/TS DPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQN 780

Query: 2341 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVFVAVTETLQMSIYHFAGLFVLLCL 2520  
SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVFVAVTETLQMSIYHFAGLFVLLCL  
Sbjct: 781 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVFVAVTETLQMSIYHFAGLFVLLCL 840

Query: 2521 GLGSALLSSLGEHAFFRLALPRIKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEBEP 2700  
GLGSALLSSLGEHAFFRLALPRIKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEBEP  
Sbjct: 841 GLGSALLSSLGEHAFFRLALPRIKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEBEP 900

FIG. 21

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

RRRSLWVLSRMCLLDPFCALVLAQVSSSSHPQPCQKRRGHAVFAGAGLQPWTT  
MEFVRALWLG--LALALGF-----SS--AGGHPPQCCGLARLGGSVRLGALLPF....  
MEFVRALWLG--LALALGF-----SS--AGGHPPQCCGLARLGGSVRLGALLPF....

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

APRFASEAQEGGFAAAQDDPESGTWRPPAPSQARWLGSALHGFPPGSRKLGGAGAAE  
APLARARA....PAALAE-----AALAPE-----  
APLARARA....PAALAE-----AALAPE-----

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

TIWPRDALFAVENLNRVEGLPYHLSLELVAIAEAGLGDPLMPFSSPSPWSSDFFV  
-----LPHNL SLELVVAAPP-----ADDPASL  
-----LPHNL SLELVVAAPP-----ADDPASL

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

LQSCHTGVVGVSAALLAFPSQGGEMICDLSSVLHIVLSHRETF--PRESQGLH  
TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL SLLREARAPLGADNPFIL  
TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL SLLREARAPLGADNPFIL

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

QLSLENSLSADAVTSRLTMNNYNFSLCCQEDWNITDFLLTNNSEKPHLESVNNH  
QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSRAG--RPPQLVLDLS  
QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSRAG--RPPQLVLDLS

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

ANLSTKDELSTFLQVQMDNIR--NSTFTLTFCCDEDSIQPFEMSTQFGSPPELHML  
RRTTGDAGLEAPLAPMAAPVGGGEAPVPAAVLLGCCDIAAPAEVLEA-----VPPGPHWLL  
RRTTGDAGLEAPLAPMAAPVGGGEAPVPAAVLLGCCDIAAPAEVLEA-----VPPGPHWLL

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

EDSONVEELREELFLVIMAHUKITQSVTHYYQDAELEVARAWDTLNFELALLFT  
STPLPPHALPTAGLPPGLLALGEVARPPLEAAIHDIVOLVARALGSAAGVQPHFALLPAT  
STPLPPHALPTAGLPPGLLALGEVARPPLEAAIHDIVOLVARALGSAAGVQPHFALLPAT

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

ENCMORKITIN-LHSQELISFLANTIFRGLGSEKVKESSTIISXNNFVFNQHPMLK  
VNCGLDLPAGPESPGCFLEARFLANTSFQGETCPVWVVTGSSQVHMSHFWWSLEDDPFGA  
VNCGLDLPAGPESPGCFLEARFLANTSFQGETCPVWVVTGSSQVHMSHFWWSLEDDPFGA

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

PLMTREDSWQGRVIMSSIIWFEQAQPHKTHFQHPNKLHRAVVTLLHHPFVFTSVVHSG  
PAWATVGSWFDGOLDLEPG---GASARPPPPQGAQVWZHLRVVTLLEHPFVFAEDPDECG  
PAWATVGSWFDGOLDLEPG---GASARPPPPQGAQVWZHLRVVTLLEHPFVFAEDPDECG

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

LCPAGQLCLDPTINDSSMLDRFSSSHSSNDVPIKTBKCCYGYCIDLLERLAEDTPDF  
QCPAGQLCLDPTINDSATLDALFAALANG--SAPRALRKCCYGYCIDLLERLAEDTPDF  
QCPAGQLCLDPTINDSATLDALFAALANG--SAPRALRKCCYGYCIDLLERLAEDTPDF

Glutamate\_Receptor\_RAT\_AAD4165  
Glutamate\_Receptor\_Human\_06039  
21659259\_IDCT3

ELYLVGDGHYGAWEHGHWTGLVGDLLSITANMAVT SFSINSARSQVVDFTSPFFSTSLGI  
ELYLVGDGHYGALEDGRWTGLVGDLLAGRAHMAVT SFSINSARSQVVDFTSPFFSTSLGI  
ELYLVGDGHYGALEDGRWTGLVGDLLAGRAHMAVT SFSINSARSQVVDFTSPFFSTSLGI

FIG. 22

21659259\_EXT\_3 MEFVRALWGLALALGPGSAGGHPPQCGVLARKLGGSVRKLGALLPRAPLAKARAKAALARA  
 21659259\_EXT\_2 MEFVRALWGLALALGPGSAGGHPPQCGVLARKLGGSVRKLGALLPRAPLAKARAKAALARA  
 21659259\_EXT\_1 MEFVRALWGLALALGPGSAGGHPPQCGVLARKLGGSVRKLGALLPRAPLAKARAKAALARA  
  
 21659259\_EXT\_3 ALAPRLPHNLSTLELVAAAPPARDPASLTRGLGQALVPPGVAALLAFPEARPELLOLHFLA  
 21659259\_EXT\_2 ALAPRLPHNLSTLELVAAAPPARDPASLTRGLGQALVPPGVAALLAFPEARPELLOLHFLA  
 21659259\_EXT\_1 ALAPRLPHNLSTLELVAAAPPARDPASLTRGLGQALVPPGVAALLAFPEARPELLOLHFLA  
  
 21659259\_EXT\_3 AATEPVLSSLRREAKAPLGAPNPFHLQLHWA SPLETLDVLVAVLQAHAWEDVGLALCR  
 21659259\_EXT\_2 AATEPVLSSLRREAKAPLGAPNPFHLQLHWA SPLETLDVLVAVLQAHAWEDVGLALCR  
 21659259\_EXT\_1 AATEPVLSSLRREAKAPLGAPNPFHLQLHWA SPLETLDVLVAVLQAHAWEDVGLALCR  
  
 21659259\_EXT\_3 TQDPGGGLVALWTSRAGRPQQLVLDLSKRD TGDAGLRAKLAPMAAPVGGEAPVAAVLGGC  
 21659259\_EXT\_2 TQDPGGGLVALWTSRAGRPQQLVLDLSKRD TGDAGLRAKLAPMAAPVGGEAPVAAVLGGC  
 21659259\_EXT\_1 TQDPGGGLVALWTSRAGRPQQLVLDLSKRD TGDAGLRAKLAPMAAPVGGEAPVAAVLGGC  
  
 21659259\_EXT\_3 DIARARRVLEAVPPGPHWLLGTPLPKALPTAGLPGLLALGEVARPPEVAIHDI VQLV  
 21659259\_EXT\_2 DIARARRVLEAVPPGPHWLLGTPLPKALPTAGLPGLLALGEVARPPEVAIHDI VQLV  
 21659259\_EXT\_1 DIARARRVLEAVPPGPHWLLGTPLPKALPTAGLPGLLALGEVARPPEVAIHDI VQLV  
  
 21659259\_EXT\_3 ARALGSAAQVQPKRALLPAPVNGGDLQPA GPE SPGRFLARFLANTSFQGR TG PVVVTGSS  
 21659259\_EXT\_2 ARALGSAAQVQPKRALLPAPVNGGDLQPA GPE SPGRFLARFLANTSFQGR TG PVVVTGSS  
 21659259\_EXT\_1 ARALGSAAQVQPKRALLPAPVNGGDLQPA GPE SPGRFLARFLANTSFQGR TG PVVVTGSS  
  
 21659259\_EXT\_3 QVHMSRHFKVWSLRDP RGA PAWATVGSWRD GQLDLEPGGASAKRP PPOGAQVWP KLRV  
 21659259\_EXT\_2 .....  
 21659259\_EXT\_1 .....  
  
 21659259\_EXT\_3 TLEHFFVFARDPDEDGQCPAGQLCLDPGTINDSATILDALFAALANGSAPRALRKC CYGYC  
 21659259\_EXT\_2 ..... PDEDGQCPAGQLCLDPGTINDSATILDALFAALANGSAPRALRKC CYGYC  
 21659259\_EXT\_1 ..... PDEDGQCPAGQLCLDPGTINDSATILDALFAALANGSAPRALRKC CYGYC



**FIG. 22 Continued**

21659259_EXT_3	RLLQARAAPAEAPPHSGRPGSQE
21659259_EXT_2	RLLQARAAPAEAPPHSGRPGSQE
21659259_EXT_1	RLLQARAAPAEAPPHSGRPGSQE

**FIG. 23**

ACGCGTTACTCCTACCAGGTTGTAGCATGCATCTTTTTGAGAGAGCAGCTGGGATCGAGTA  
TACTCTTGACTTAAATATGTTTGTITATAAAGACAAATGGAGAAATCAATTTTTTCCCTGA  
ATTCTTAGGAGCACTTTAGTGAATAAAGAACCTGACAGTATGCTGGCCACATGTTTAAGG  
ACAAAGGTGTCTGGGGAAATAAGCAAGATCATAGAGGAGCTTTCTTAATTGACCGAAGTCC  
TGAGTACTTCGAACCCATTTTGAACACTTTCGTCATGGACAGCTCATTGTAAATGATGGCA  
TTAATTTATTGGGTGTGTTAGAAGAAGCAAGATTTTTTGGTATTGACTCATTGATTGAACAC  
CTAGAAGTGGCAATAAAGAATTCTCAACCACCGGAGGATCATTACCAATATCCCGAAAGG  
AATTTGTCCGATTTTTGCTAGCAACTCCAACCAAGTCAGAACTGCGATGCCAGGGTTTGAA  
CTTCAGTGGTGCTGATCTTTCTCGITTTGGACCTTCGATACATTAACCTTCAAAATGGCCAATT  
TAAGCCGCTGTAATCTTGACATGCAAATCTTTGCTGTGCAAATCTTGAACGAGCTGATCTC  
TCTGGATCAGTGCTTGACTGTGCGAATCTCCAGGGAGTCAAGATGCTCTGTTCTAATGCAG  
AAGGAGCATCCCTGAAACTGTGTAATTTTGAGGATCCTTCTGGTCTTAAAGCCAATTTAGA  
AGGTGCTAATCTGAAAGGTGTGGATATGGAAGGAAGTCAGATGACAGGAATTAACCTGAG  
AGTGGCTACCTTAAAAAATGCAAAGTTGAAGAACTGTAACCTCAGAGGAGCAACTCTGGC  
AGGAACTGATTTAGAGAATTGTGATCTGTCTGGGTGTGATCTTCAAGAAGCCAACCTGAGA  
GGGTCCAACGTGAAGGGAGCTATATTTGAAGAGATGCTGACACCACTACACATGTCACAAA  
GTGTCAGATGAGAATTTTAGGGGCTGGAGGAAGATGTAAAAGATGAAAATGTTTTCTTAT  
CACTTTTCTTTCTCCACCCACTCAGTTGTCTAGAAGAAATAACACTGTAAGGAAATTTAAAA  
AAAAAAAA

**FIG. 24**

MLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLEEARFFGID  
SLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGLNFSGADLSRLDLRYINFKMAN  
LSRCNLAHANLCCANLERADLSGSVLDCANLQGVKMLCSNAEGASLKLCNFEDPSGLKANLE  
GANLKGVDMEGSQMTGINLRVATLKNAKLKNCNLRGATLAGTDLENCDSLGCDDLQEANLRGS  
NVKGAIFFEMLTPLHMSQSVR

FIG. 25

Score = 1486 (523.1 bits), Expect = 1.4e-151, P = 1.4e-151  
Identities = 286/286 (100%), Positives = 286/286 (100%), Frame  
= +1

```
Query: 130 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 309
      RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI
Sbjct: 104 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 163

Query: 310 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLLATPTKSELRCQGL 489
      NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLLATPTKSELRCQGL
Sbjct: 164 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLLATPTKSELRCQGL 223

Query: 490 NPSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGGSVLD CANLQGVKMLCS 669
      NPSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGGSVLD CANLQGVKMLCS
Sbjct: 224 NPSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGGSVLD CANLQGVKMLCS 283

Query: 670 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLNKCNLRGA 849
      NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLNKCNLRGA
Sbjct: 284 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLNKCNLRGA 343

Query: 850 TLAGTDLENCDSLGC DLQEANLRG SNVKGAI FEEMLTPLHMSQSVR 987
      TLAGTDLENCDSLGC DLQEANLRG SNVKGAI FEEMLTPLHMSQSVR
Sbjct: 344 TLAGTDLENCDSLGC DLQEANLRG SNVKGAI FEEMLTPLHMSQSVR 389
```

**FIG. 26**

TTTCAGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAACATGCAT  
GGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCCTTAAGATCTCACCAAAGCCCAGCAAACCACTGAGGCCT  
TGTATTCAGCTGAGCAGCAAGAATGAAGCCAGTGGAATGGTGGCCCCGGCTGTCCAGGAGAAGAAGGTGA  
AAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTGGCCCTGACAATGGTCAAAGTGTTCGGAATTCGA  
TGACCCGCTAGATATGCCATTCAACATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAG  
AGCGAGAGCTTTGTTCTGGATTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGG  
CCGACCACGTCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCCTGTGAAGGTTTCAGAA  
CCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGCTACACAGACTTTCCT  
TGTCAGTACGTGAAGGACACTTATGCCGGTTCAGACAGGGACACGTTCTCCTTCGACATCAGCTTGCCCG  
AGAAGATTAGTCTTATGAAAGAATGGAGTTTGCTGTGTACTACGAGTGCAATGGACAGACGTACTGGGA  
CAGCAACAGAGGCAAGAATATAGGATCATCCGGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCC  
CACAGTGGACCGGATTTGGGAATATCCTTTGACCAGTTCGGAAGCCCTCGGTGTTCTATGGTCTGTTTC  
CAGAGTGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGACTGCAGGTGACAGGGCG  
TGGCGGAGCTGCCACA

**FIG. 27**

MMAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKKVKKRVSPADNQG  
LALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADYLDFRNRLQADHVCLENCVL  
KDKAIACTVKVQNLAFEKTVKIRMTFDTWKS YTD FPCQYVKDTYAGSDRDTFSFDISLPEKIQSYERMEF  
AVYYECNGQTYWDSNRGKNYRIIRAELKSTQGMTKPHSGPDLGISFDQFGSPRC SYGLFPEWPSYLGYEK  
LGPYY

FIG. 28

Score = 3195 (479.4 bits), Expect = 2.8e-138, P = 2.8e-138  
Identities = 763/903 (84%), Positives = 763/903 (84%), Strand = Plus / Plus

```

Query:      6 AGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAAC 65
            AG TTCTAGCCTG C TCTA C TGATGGC GTGGACAT GA TACAG TACA C
Sbjct:     65 AGACTTCTAGCCTGCCCTCTAACG---TGATGGCCGTGGACATAGAATACAGCTACAGC 121

Query:     166 TGCATGGCTCCTTCTCTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACAAAGCCCAGC 125
            G ATGGC CCTTC TCGC AGAG G TT CCTT AAGATCTC CC AA C A C
Sbjct:    122 AGTATGGCCCCCTTCTCTGCGCAGAGAGCGCTTCACCTTCAAGATCTCCCCCAAAGTGAAC 181

Query:     126 AAACCACTGAGGCCCTTGTATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGAATGGTGGCC 185
            AA CCACTGAGGCCCTTGTATTTCAGCTG GCAGCAAG ATGAAGCC G GAATGGTGGCC
Sbjct:    182 AAGCCACTGAGGCCCTTGTATTTCAGCTGGGCAGCAAGGATGAAGCCGGCAGAATGGTGGCC 241

Query:     186 CCGCTGTCCAGGAGAAGAAGGTGAAAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTG 245
            CC C GT CAGGAGAAGAAGGTGAA AAGCGGGTGTCTTCGC GACAACCAGGGGCTG
Sbjct:    242 CCCACAGTACAGGAGAAGAAGGTGAAAGAAGCGGGTGTCTTCGCCGACAACCAGGGGCTG 301

Query:     246 GCCCTGACAATGGTCAAAGTGTCTCGGAATTCGATGACCCGCTAGATATGCCATTCAAC 305
            GCCCT ACAATGGT AAAGTGTCTCGGAATTCGATGACCC CTAGATAT CC TT AAC
Sbjct:    302 GCCCTAACAATGGTCAAAGTGTCTCGGAATTCGATGACCCACTAGATATTCGGTTTAAC 361

Query:     306 ATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAGAGCGAGAGCTTTGTT 365
            ATCAC GAGCTCCTAGACAACAT GTGAG TGACGACAGCAGAGAG GAGAGCTTTGTT
Sbjct:    362 ATCACTGAGCTCCTAGACAACATCGTGAGTCTGACGACAGCAGAGAGTGAAGCTTTGTT 421

Query:     366 CTGGATTTTTCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGGCCGAC 425
            TGGATTTT C CAGCC TCTGCAGATTACTTAGACTTTAGAAATCG CTTCAG CC AC
Sbjct:    422 TTGGATTTTTCAGCAGCTTCTGCAGATTACTTAGACTTTAGAAATCGGCTTCAGACCAAC 481

Query:     426 CACGTCCTGCTTGAAGAACTGTGTGCTCAAGGACAAGGCCATTGACGGCACTGTGAAGGT 485
            CA GTCTGCCT GA AACTG GTGCT AAGGA AA GCCAT GC GGCAC GT AAGGT
Sbjct:    482 CATGCTCGCCTCGAAAACCTGCGTGTGAAGGAGAAGCCATCGCGGCACCGTCAAGGTC 541

Query:     486 CAGAACCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTGACACCTGGAAGAGC 545
            CAGAACCT GCATT GAGAAG GTGAA AT AG ATGAC TTGCA ACCTGGAA AGC
Sbjct:    542 CAGAACCTGGCATTTGAGAAGGTTGTGAAGATCAGCATGACATTGATACCTGGAAAAGC 601

Query:     546 TACACAGACTTTCTTGTGTCAGTACGTGAAGGACACTTATGCCGGTTTCAGACAGGGACACG 605
            T CACAGACTT CCTTGTGCTAGT GTGAAGGACACTTA GC GGTTCAGACAGGGACAC
Sbjct:    602 TTCACAGACTTCCCTTGTGTCAGTATGTGAAGGACACTTACGCTGGTTTCAGACAGGGACACA 661

Query:     606 TTCTCCTTCGACATCAGCTTGCCCCGAGAAGATTAGTCTTATGAAAGAATGGAGTTTGCT 665
            TTCTCCTT GA ATCAGC T CC GAGAA AT CAGTCTTATGAAAGAATGGAGTT GC
Sbjct:    662 TTCTCCTTGTATATCAGCTACCGGAGAAAATCCAGTCTTATGAAAGAATGGAGTTTCGCC 721

Query:     666 GTGTACTACGAGTGCAATGGACAGACGTAAGGACAGCAACAGAGGCAAGAACTATAGG 725
            GTGT CTACGAGTG AA GG CAG CGTACTGGGACAGCAACA AGGCAA AACTA AGG
Sbjct:    722 GTGTGCTACGAGTGTAACGGCCAGTCTGACTGGGACAGCAACAAAGGCAAAAACACTACAGG 781

Query:     726 ATCATCCGGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCCCACAGTGGACCGGAT 785
            ATCA C GGGC GA T A ATC ACCCAGGGAATGAC AGCC ACA TGG CCGGAT
Sbjct:    782 ATCACCAGGGCCGAACCTCAGATCCACCCAGGGAATGACTGAGCCGTACAATGGGCCGGAT 841

Query:     786 TTGGGAATATCCTTTGACCAGTTTCGGAAGCCCTCGGTGTTCCTATGGTCTGTTTCCAGAG 845
            TT GGAAT TC TTTGACCAGTTTCG AGCCCTCGGTGTTCCT GG CTGTTTCCAGAG
Sbjct:    842 TTTGGAATCTCTTTGACCAGTTTCGGGAGCCCTCGGTGTTCCTTCGGCCTGTTTCCAGAG 901

Query:     846 TGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGA-----CTGCAGG 900
            TGGCC AGTTA T GG TATGAAAAGCT GGGCCCTA TACTAGTGA CTGCAG
Sbjct:    902 TGGCCTAGTTATCTGGGGTATGAAAAGCTGGGGCCCTATTACTAGTGAGTTGACTGCAGT 961

Query:     901 TGACAG 906
            TGACAG
Sbjct:    962 TGACAG 967

```

FIG. 29

Score = 1366 (480.9 bits), Expect = 1.3e-139, P = 1.3e-139  
Identities = 255/284 (89%), Positives = 270/284 (95%)

Query: 2 MAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKVKK 61  
MAVDIEY Y+ MAPSLR+ERF FKISPK +KPLRPCIQL SK+EA MVAP VQEKVKK  
Sbjct: 1 MAVDIEYSYSSMAPSLRRERFTFKISPKLNKPLRPCIQLGSKDEAGRMVAPTQEKVKK 60

Query: 62 RVSFADNQGLALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADY 121  
RVSFADNQGLALTMVKVFSEFDDPLD+PFNITELLDNIVSLTTAESESFVLDF QPSADY  
Sbjct: 61 RVSFADNQGLALTMVKVFSEFDDPLDIPFNITELLDNIVSLTTAESESFVLDFPQPSADY 120

Query: 122 LDFRNRLQADHVCLENCVLKDKAIAGTVKVQNLAFETVKIRMTFDTWKS+TDFFPCQYVK 181  
LDFRNRLQ +HVCLENCVLK+KAIAGTVKVQNLAFET VKIRMTFDTWKS+TDFFPCQYVK  
Sbjct: 121 LDFRNRLQTNHVCLENCVLKEKAIAGTVKVQNLAFETVKIRMTFDTWKS+TDFFPCQYVK 180

Query: 182 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVYECNGQTYWDSNRGKNYRI IRAELKSTQ 241  
DTYAGSDRDTFSFDISLPEKIQSYERMEFAV YECNGQ+YWDSN+GKNYRI RAE+STQ  
Sbjct: 181 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVCYECNGQSYWDSNKGKNYRITRAELRSTQ 240

Query: 242 GMTKPHSGPDIGISFDQFGSPRCSYGLFPEWPSYLGYEKLGPPY 285  
GMT+P++GPD GISFDQFGSPRCS+GLFPEWPSYLGYEKLGPPY  
Sbjct: 241 GMTPEYNGPDFGISFDQFGSPRCSFGLFPEWPSYLGYEKLGPPY 284



FIG. 30

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

```

Q63759_PP1_RAT      .....MAMDIEYSYSSMPSLR..RERFTFISPKLNFLMPCYCLG
AC016485_A          .....MAMDIEYRYNCMSPLR..QERAFKISPKPSPLPCCLIS
O08541_PP1_MOUSE    .....MAMRICLAHSPPLKSFLEPYNGFCRNFVNLNPLDQSSV.
AAD33215_PPP1R5_HUMAN MIQVLDPRPLTSSVMPVDVLMRRECLAHSEPVKSFLEPYNEFCRNFVNLNPLDQSSV.

Q63759_PP1_RAT      SHDEAGRMVAPTVCCKVKKVVSADNQSLALTMKKVFSDFDP..LQMPENITILLNI
AC016485_A          SHDEAGSMVAPAVCKVKKVVSADNQSLALTMKKVFSDFDP..LQMPENITILLNI
O08541_PP1_MOUSE    -HQEANSQSEWSPHNQAARKVVFADSKSLSLTAHHVFSGLPPEPAWQLQDYLQNLNIS
AAD33215_PPP1R5_HUMAN -SHKAKSQNDWECSHNQAARKVVFADSKSLSLTAHHVFSGLPPEPAWQLQDYLQNLNIS

Q63759_PP1_RAT      VSLTTAESSESFVLDFPQPSADYLDERNRLQTHVCLENGVLHMAAASVVEVCHAFENV
AC016485_A          VSLTTAESSESFVLDFSPSADYLDERNRLQADHVCLENGVLHMAAASVVEVCHAFENV
O08541_PP1_MOUSE    SSKLHHEEKNLWDFDFPQPSDYLSERDFQRNFVCLENGSEEDTITGVVWKMSFEKK
AAD33215_PPP1R5_HUMAN SSKLHHEEKNLWDFDFPQPSDYLSERDFQRNFVCLENGSEEDTITGVVWKMSFEKK

Q63759_PP1_RAT      VKLRMTFDTWKSHTDFPQPSADYLDERNRLQTHVCLENGVLHMAAASVVEVCHAFENV
AC016485_A          VKLRMTFDTWKSHTDFPQPSADYLDERNRLQADHVCLENGVLHMAAASVVEVCHAFENV
O08541_PP1_MOUSE    VQARRTFDTWKSHTDFPQPSADYLDERNRLQTHVCLENGVLHMAAASVVEVCHAFENV
AAD33215_PPP1R5_HUMAN VQARRTFDTWKSHTDFPQPSADYLDERNRLQADHVCLENGVLHMAAASVVEVCHAFENV

Q63759_PP1_RAT      SYWDSKCKKNYRITRAELR..STGMIETYN.....SDFDGLSDFDQFGSPSCSYDLFPE
AC016485_A          SYWDSKCKKNYRITRAELR..STGMIETYS.....SDFDGLSDFDQFGSPSCSYDLFPE
O08541_PP1_MOUSE    IYWDNNEGQNYRIVHVQWPEQGVETQVAKDCARQGGPKTEPTVFGSPRLASGLFPE
AAD33215_PPP1R5_HUMAN VYWDNNDGQNYRIVHVQWPEQGVETQVAKDCARHTSPKTEESTIEGSPRLASGLFPE

Q63759_PP1_RAT      WPSGLGYEKLGPY
AC016485_A          WPSGLGYEKLGPY
O08541_PP1_MOUSE    WPSGRVENLTSR
AAD33215_PPP1R5_HUMAN WPSGRMENLTSR

```

**FIG. 31**

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGC  
TACTACCGCTTTGTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATC  
AGCTTGGCTGTGCGGAAGATCGCGCTGCTGCTGAAGCCGGACAAGGAGATCGAACA  
CCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTTCCGAAACTACACTGTGC  
AGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGAAAA  
TGCCAGATCTCATTCGTTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCC  
CCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGG  
CTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAAGACTGCCACCTCCACAAGGGC  
TTCTGGCCCTCTACCAAACCGTGGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGGC  
TGGGGACTCAGGGACACCTGGGCTGGATCCCAGCCCTGCC

**FIG. 32**

**MPPNLTGYR FVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFR  
NYTVQFDVGVEFEEDLRSVDGRKCQISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSL  
RLTFRTQPSSSENKTAHLHKGFLALYQTVALSGLSDS**

### FIG. 33

Score = 355 (125.0 bits), Expect = 1.0e-31, P = 1.0e-31  
Identities = 68/70 (97%), Positives = 70/70 (100%), Frame = +2

```
Query:   38 MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217
          MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN
Sbjct:   1 MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query:   218 YTVQFDVGVE 247
          YT+QFDVG+
Sbjct:   61 YTLQFDVG+ 70
```

**FIG. 34**

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGCTACTACCGCTTT  
GTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATCAGCTTGGCTGTGCGGAAGATCGCGC  
TGCTGCTGAAGCCGGACAAGGAGATCGAACACCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTT  
CCGAAACTACACTGTGCAGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGA  
AAATGCCAGACCATAGTAACCTGGGAGGAGGAGCACCTGGTGTGTGTGCAGAAAGGGGAGGTCCCCAACC  
GGGGCTGGAGACACTGGCTGGAGGGAGAGTTGCTGTATCTGGAACCTGACTGCAAGGGATGCAGTGTGCGA  
GCAGGTCTTCAGGAAGGTCAGATAGCCGGAGAGGAGCCAAGATCCCTCCAGACAGCACCAGCTCACAGAC  
GCTCTTGTTGTGCCCCCTTCAAGCCCAGATTGTGCCAGATCTCATTTCGTTCGGTTCGGATCCAAGCCAGTT  
CTGTGGTCAGCAAGGCTCCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGT  
TTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCACCTCCACAAGGGCTTCCTGG  
CCCTCTACCAAACCGTGGGTGAGTGTCCCTCCTGGGGGTGCAGGGAGGGAGCCTCTGTTCACGCCATGA  
CCCTGGTATCTTCAAGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGG

**FIG. 35**

MPPNLTGYRFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVGVE  
FEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGELLYLELTARDAVCEQVFRKVR

# FIG. 36

Score = 712 (250.6 bits), Expect = 1.5e-69, P = 1.5e-69  
Identities = 133/135 (98%), Positives = 135/135 (100%), Frame =  
+2

```
Query:   38 MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217
          MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN
Sbjct:   1  MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query:   218 YTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGEMLYLEL 397
          YT+QFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGE+LYLEL
Sbjct:   61 YTLQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGEMLYLEL 120

Query:   398 TARDAVCEQVFRKVR 442
          TARDAVCEQVFRKVR
Sbjct:   121 TARDAVCEQVFRKVR 135
```

FIG. 37

C018653\_A MPPNLTGYVRFVSOQNMEDYLQALNISLAVKIALLLKPDNEIEHQCNIHMTVRTLSTFRN  
C018653\_dal\_ MPPNLTGYVRFVSOQNMEDYLQALNISLAVKIALLLKPDNEIEHQCNIHMTVRTLSTFRN

C018653\_A YTVCFDVGVEFEEDLRSVDGRHCCISFVGSIPSQFEGQISPLQPPCQREFVRSRSR  
C018653\_dal\_ YTVCFDVGVEFEEDLRSVDGRHCCITIVTWEEHLVVKKEVPNE--LWEHHE-DEELY

C018653\_A LTFRTQPSSSENKTAHLHGFLLALYOTVALSGSLSDS  
C018653\_dal\_ LELTARDAVCEQVFRKV-----